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⑪ Publication number: **0 679 716 A1**

⑫

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158(3) EPC

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⑤ GENE SIGNATURE.

⑦ A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

EP 0 679 716 A1



Table 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.  
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku  
(C) CITY: Tokyo  
(E) COUNTRY: JAPAN  
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS  
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916  
(B) FILING DATE: 11. November 1994

SEQ ID NO:111  
SEQUENCE LENGTH:375  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60  
GATTATGAAA TGTCCCCTCA AACTCATTGC AGCAGATAAC TTTTGTGAGT CATTGACTTC 120  
ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180  
ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTTCTATG 240  
GCTTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTTT 300  
ACTGTCAGNT TAANTTACAG CTTTATGGG TGGTAACTT TTCGTNCATT TTCAAAAAAN 360  
CCNGGGGNNN NNNNN 375

SEQ ID NO:112  
SEQUENCE LENGTH:356  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTGA AAATTCATT GTATACTTTT GTTTNATCT AGGACTTCAT 60  
GTTTTTNAAG AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120  
AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180  
TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTGATAC TTTTCCTTTT CAAATTATAG 240  
TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTGACA TTTNTNAATA CTCATTGTCA 300  
ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113  
SEQUENCE LENGTH:351  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60  
GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120  
GCTAGGATAT AACCCCCAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180  
TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240  
TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTGA GTGATTTACA TGTACATTTT 300  
ATAGGGGACA TGTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114  
SEQUENCE LENGTH:352  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00128

5 SEQ ID NO:7844  
SEQUENCE LENGTH:37  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGCT 37

10 SEQ ID NO:7845  
SEQUENCE LENGTH:37  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
15 TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

20 SEQ ID NO:7846  
SEQUENCE LENGTH:38  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
25 TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

30 SEQ ID NO:7847  
SEQUENCE LENGTH:22  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
35 TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CCAGGGTTTT CCCAGTCACG AC 22

40 SEQ ID NO:7848  
SEQUENCE LENGTH:22  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
45 TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
TCACACAGGA AACAGCTATG AC 22

## 50 Claims

- 55 1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.



2. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 1

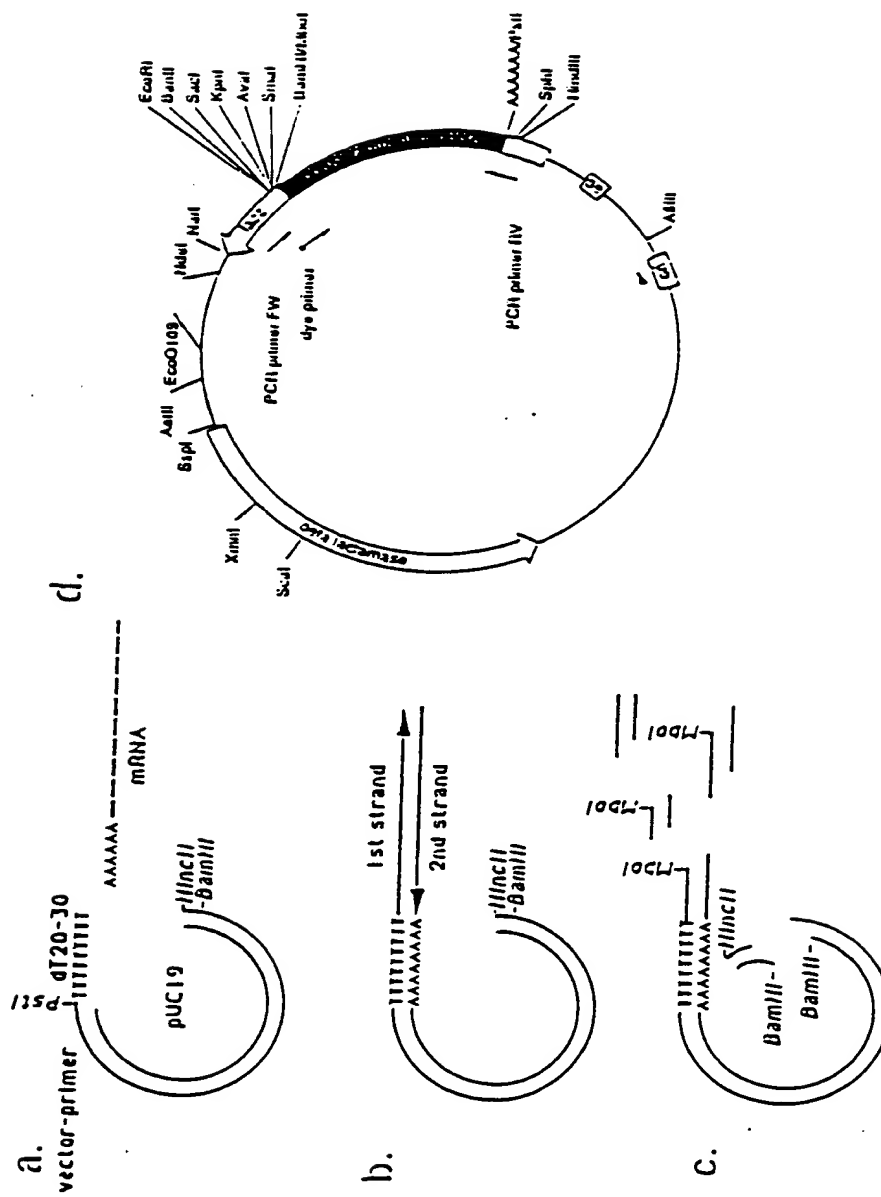


Fig. 2

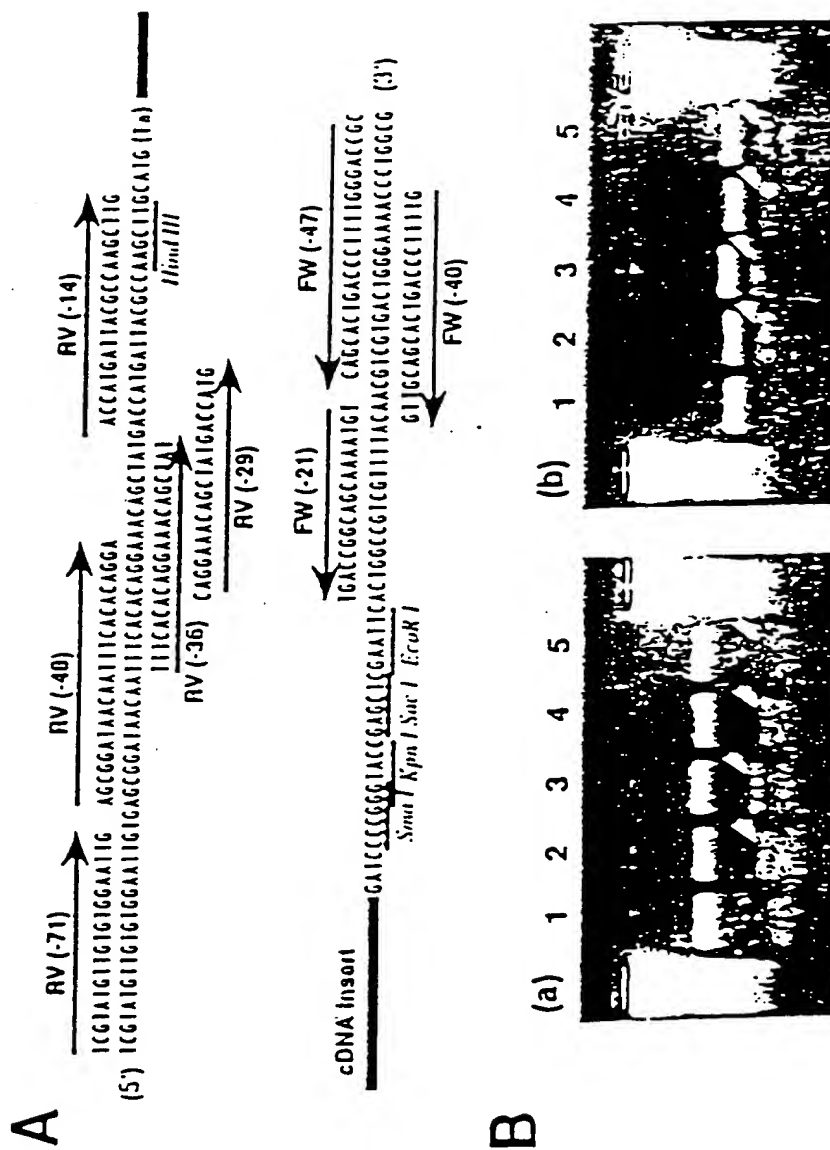


Fig. 3

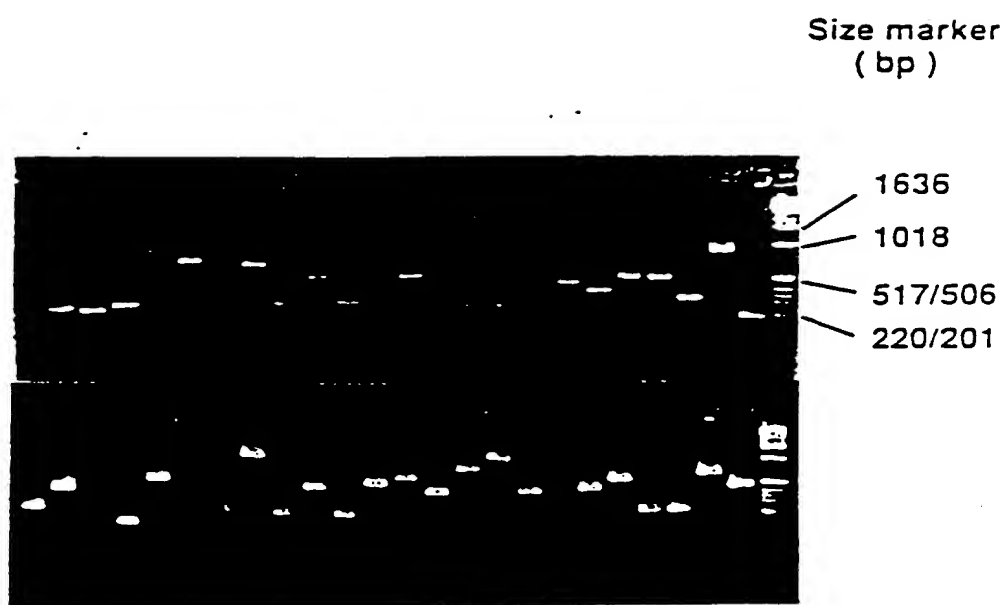


Fig. 4

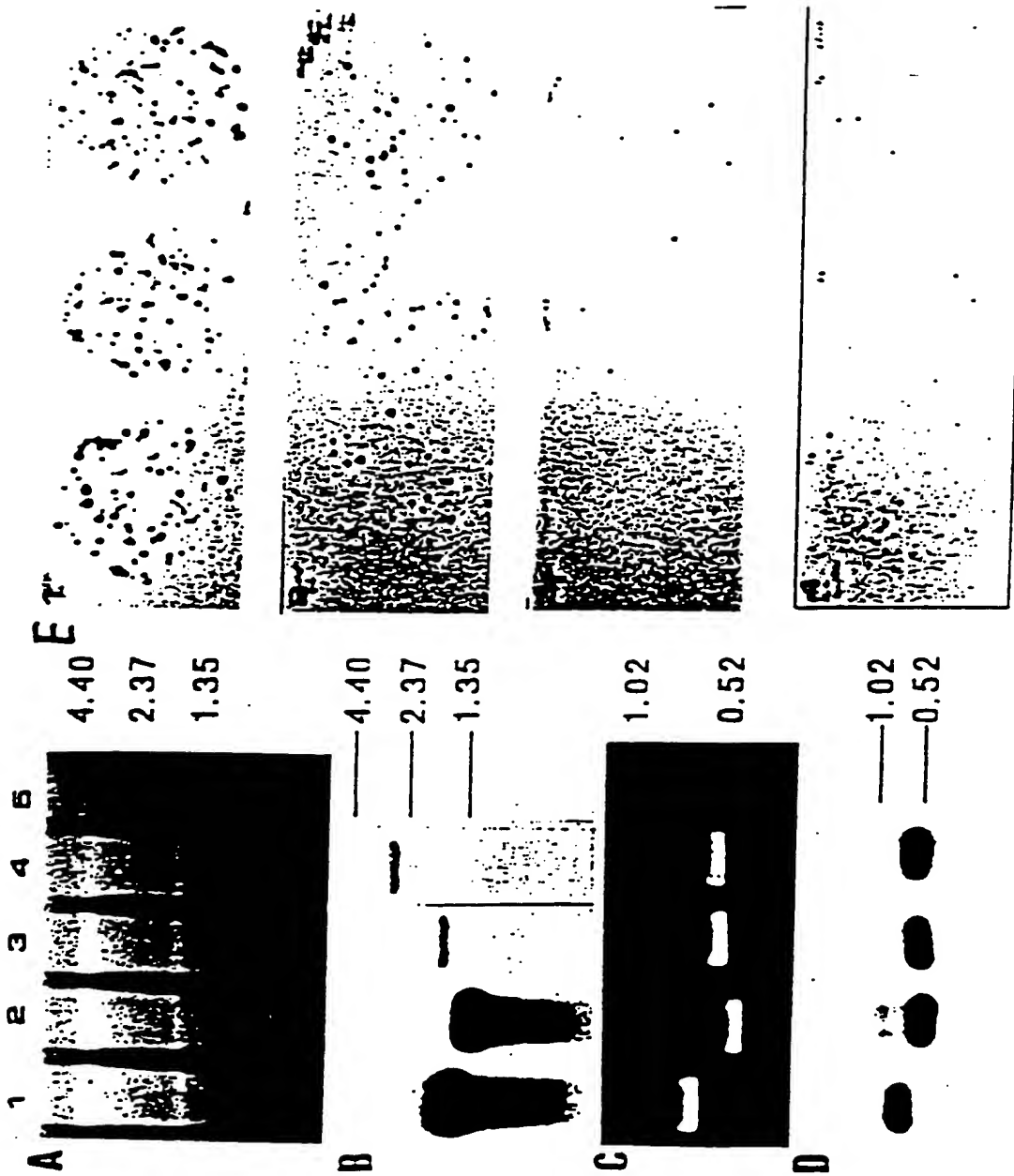


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- $\alpha$	$\alpha$ 1-andrypsin	H <sub>2</sub> RNP core protein A1	Inter- $\alpha$ -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

## Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A			B			C		
			ln 982 (%)			"in 8,000 (%)"			"in 26,400 (%)"		
I	a15	Elongation factor - 1A $\alpha$	22 (2.2)			307 (3.5)			NT		
	c321	Translationally restricted tumor protein	12 (1.2)			89 (1.0)			NT		
	ib030	$\alpha$ -1-antitrypsin	8 (0.8)			119 (1.4)			NT		
	hm01b02	Light chain of ferritin	6 (0.6)			62 (0.7)			NT		
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)			27 (0.3)			NT		
	hm02d02	Ribosomal protein S11	3 (0.3)			29 (0.3)			NT		
	ib042	Human RNP core protein A1	2 (0.2)			7 (0.1)			NT		
	s155	unknown	1			2			5 (0.02)		
II	s159	unknown	1			2			4 (0.02)		
	s639	unknown	1			1			3 (0.01)		
	s635	unknown	1			0			2 (0.01)		
	s170	unknown	1			0			1 (0.004)		
	s154	unknown	1			0			1 (0.004)		
	s167	unknown	1			0			1 (0.004)		
	s645	unknown	1			0			1 (0.004)		
	s647	unknown	1			0			0 (<0.004)		
	s632	unknown	1			0			0 (<0.004)		

Fig. 6

GS		Chromosomal position		Sequences of primers		AT		HO		HE		HO		CO		G		T	
CII		Séq		Anti-séq															
91600700	pin2166	1	CAGAGCCCCAGTACACTAT	1	AAGTTATGTGGGGTCAG	40	114	114	115	104	110	104	110	104	110	1	2	1	2
91601026	pin2144	1	AATGGGACAGTTACACTGA	1	CCAGCTTCCTTGACTTGAGA	40	03	04	04	>200	>200	>200	>200	>200	>200	1	1	1	1
91601075	pin0003	1	TGGACTGTGGATACCTATCT	1	ACAGTACCCCTGAAATGGCT	40	124	124	124	103	107	103	107	103	107	4	4	4	4
91601607	pin1772	1	GTCACTCTCAGCCATAGCAC	1	ACCATCTCAGCCACACAT	50	104	104	104	180	>200	180	>200	180	>200	6	6	6	6
91601094	pin0347	1	GCCCCAACAGAGGAACCTC	1	TAATTCACCTCCCGTAAC	51	114	114	116	>200	200	>200	200	>200	200	1	1	1	1
91601116	pin1771	1	GGGTTTCAATAGGGTGTAGACC	1	GCCCCAATCTGTCAAACTG	48	95	95	95	70	107	70	107	70	107	1	1	1	1
91601191	pin0609	1	TGGTGGATGTAACTTTTG	1	GGCTGAACATCAGCTCTTG	47	97	97	97	200	200	200	200	200	200	1	1	1	1
91601200	pin1251	1	TAAAGAGACCTTATGGAGACC	1	AATACTTGGTTAGTCACITAC	47	97	97	98	200	200	200	200	200	200	1	1	1	1
91601346	pin0902	1	TCAGGTCTGCTGGAGGATG	1	AATCAGACAGCAGATTTTG	53	120	122	122	>200	>200	>200	>200	>200	>200	1	1	1	1
91601446	pin1510	1	AAGGTGTACAGGATATTGCCAGA	1	TGCAATAGCCCATCTCAT	47	130	125	125	>200	>200	>200	>200	>200	>200	1	1	1	1
91601464	pin1438	1	CCAAAGACCTCCGTTGAACA	1	TTGGGAGAGCCATAGACAG	51	100	100	100	>200	>200	>200	>200	>200	>200	1	1	1	1
91601460	pin0427	1	TACTCAGTGGAAAGATAAAC	1	CAGTGGACACATTTCTTA	40	90	90	90	200	200	200	200	200	200	1	1	1	1
91601521	pin2705	1	CCCAATCAATTTGTTAAATG	1	TTTGAATCAGAGACATGAAGTT	43	102,115	100	100	>200	>200	>200	>200	>200	>200	2	2	2	2
91601554	pin2291	1	CCAGAGAGTTCAGGGATG	1	GGTACAAAGTGGCAAATGACT	46	57	57	57	78	155	78	155	78	155	1	1	1	1
91601572	pin2005	1	CCAACATGTTCCAGGATG	1	AAACAGTAGTCCACAGCAT	44	58	58	58	>200	>200	>200	>200	>200	>200	4	4	4	4
91601620	pin1350	2	CATGATCTCTGGTGGTA	2	CCGTTATGCTACATGCT	46	04	04	04	109	109	109	109	109	109	1	1	1	1
91601636	pin1730	2	AGGCTAAATGTCGCTGCT	2	AAACAGTAGTCCACAGCAT	46	04	04	04	109	109	109	109	109	109	1	1	1	1
91601650	pin0931	2	AAAGCAATCAAAATACCAA	2	TTCAATATGTTAACCACTA	40	90	90	90	115	115	115	115	115	115	1	1	1	1
91601671	pin0925	2	TAATGTACCAAGTGAATAG	2	TAATGTAAATATGAGGTAA	45	08	08	08	200	200	200	200	200	200	1	1	1	1
91601713	pin2010	2	CCAGATGGAAGGGAAGTCT	2	CTGGAATATGAGGAATCAACAG	47	125	125	125	150	150	150	150	150	150	1	1	1	1
91601752	pin0935	2	TCAGATTTGCTCTAATAA	2	GGAAATATCGCTTCAGTTG	43	103	103	103	200	200	200	200	200	200	1	1	1	1
91601760	pin2003	2	AGTCTCTTGGCTCTCAT	2	TATCCTCAGTGGCTTTATG	52	137	137	137	200	200	200	200	200	200	1	1	1	1
91601830	pin2435	2	TTTGTACCTAGCTAAGATACTT	2	ATCCGTGCCACACATAGTGA	45	105	105	105	200	200	200	200	200	200	1	1	1	1
91601842	pin1671	2	TTATAGGGAGTATATCTCTG	2	AGTCCATCTCCACATG	45	67	65	65	>200	>200	>200	>200	>200	>200	1	1	1	1
91601853	pin1245	2	TGCTTTCCGCTCTAAGT	2	ATGTACAATTTGGGTATGTAGG	45	75	75	75	170	190	170	190	170	190	1	1	1	1
91601875	pin1246	2	ATCTAGTTTGTGAAGTG	2	ACTGATTTGGTCCCATCTG	44	60	67	67	200	200	200	200	200	200	1	1	1	1
91601901	pin0440	3	CGAACATTTCACTCTCATA	3	ATGATTTATTTAGGACGAA	43	60	60	60	200	200	200	200	200	200	3	3	3	3
91601910	pin1750	3	TCGGGCTCTTGGTGTGGA	3	GGCCACTGAGTACAATGTC	51	115	115	115	200	200	200	200	200	200	1	1	1	1
91601920	pin2434	3	AAAGAAAGCACACTGGCTAA	3	ATGTATAGACAATCCAAAG	42	90	90	90	200	200	200	200	200	200	1	1	1	1
91601930	pin0660	3	GTAGTCTCTGGCTTTAGC	3	AAGCATTTGATTTCTTACAT	43	77	77	77	200	200	200	200	200	200	1	1	1	1
91601977	pin1728	3	GGTCTGTTATTTTACAT	3	AAACAAGAGGATGGTTCAGA	43	75	75	75	155	155	155	155	155	155	1	1	1	1
91601986	pin1022	3	GATCCTTGGTGTAGTTCAGTC	3	CTGCAAAATACAGGGAATCAT	46	83	83	83	160	160	160	160	160	160	1	1	1	1
91601991	pin2209	3	ACCCAGTCCCAATCCAGT	3	ACACTCCCCAGCCCTTACT	55	105	105	105	113	113	113	113	113	113	1	1	1	1
91601996	pin2455	3	ATCTAGTGGCTGTAGTAT	3	TAAAGAGATGAATTTATGGT	42	130	130	130	190	190	190	190	190	190	1	1	1	1
91602011	pin1253	4	GTCTTGTCTATCTCTGTA	4	AAGCATTTATTTAGGTTTA	43	90	90	90	200	200	200	200	200	200	1	1	1	1



Fig. 7

91000148	pm2256	4	GGCCAAAGTTCTCTAGTAT	GTCCAGTTTATTCAGAGCA	42	62	62	62	69	1	2
91001052	pm1151	4	GTCCATGCCTGTGTAT	GTATATATCCATCATCA	43	80	80	-	-	1	1
91001215	pm0988	4	AGAAATTAATAGCATAGT	TAGAGTCAAGTTCCTGTG	43	100	100	130	-	1	1
91001298	pm1267	4	ATCAAGTTTATTCCTCA	CATCCATCATACACAGTC	43	116	116	>200	180	1	1
91000993	pm0901	5	TCTCGTGAAGAGCAGCACA	TCTAAGGAMGACAGATC	49	101	102	113	200	1	1
91000598	pm1809	5	AGCAATGCCCTTATCCACAG	CTAAGAGCTTGAACCTTCAT	45	87	87	>200	>200	1	1
91001085	pm0319	5	TACCCAGATAATTACAGT	GATACATAGCAGGTAAAGT	44	120	120	-	-	1	1
91001101	pm2264	5	ATTTGTAGTGGTTTACTA	AGACAAATATCCCAAGC	47	89	89	100	>200	1	1
91001461	pm1160	5	ATTTGTAGTGGTTTACTA	AGAAATGGATCTTTATTC	43	101	99	>200	>200	1	1
91000353	pm2720	6	ATGTGATAGTCTCTTCA	TGCATCCCTCAATGCTCT	44	78	78	72	>200	2	3
91001226	pm1151	6	CATTGACAGCAGCAGACAG	CTGGCCCTCTCTCTAGTA	53	102	104	145	200	1	1
91001134	pm1216	6	TAGGCAAAACAGGAGAGAG	AAGGAGCTGGTCTCAGTTC	48	65	65	110	>200	1	1
91001457	pm1785	6	TATATGCAATATCCAAAGTCTG	TCTAATATTCGGTCCCTAIGT	46	90	90	>200	>200	1	1
91001523	pm0285	6	TTGTACGTTGTCTGTCAGT	TTTAAATGTCTAGTAAAT	42	86	70	>200	100	1	1
91001525	pm0228	6	GCACCTAGCCCTCCAAAGT	TATATATCAGTCCAGAGC	49	138	138	>200	>200	1	1
91001562	pm2619	6	TCTGCATTGACAGGAGCCAG	TTTGAGATTTAATGATCATTC	43	62	62	>200	45	1	1
91000624	pm0991	7	GACCTGAAGTGTGAATGAGT	AACCTAGCTTATGGGATTT	45	119	119	>200	-	1	2
91001145	pm0281	7	AGCCAAAGTCGGGTCTGCT	CCACGGACAGGTGAGTCAT	56	159	155	115	>200	4	4
91001169	pm0219	7	AATCATTTGGGAGAGCTGTA	AAGACAAGTTTATCCAGACA	45	88	83	130	-	1	1
91001578	pm1101	7	TCAGGCAGTCTGCTCAGATA	TTTGCAGGTAACTGTTTA	44	77	76	170	-	1	1
91001207	pm0956	8	AACAGTATTCGTTGTCAGACTAG	TCCATTAATAGCCAGTCTCAG	47	81	81	105	70	1	1
91001176	pm2527	9	TTCCCTAATGTTGTTCTAC	AAACACAGAACACACTAAG	48	93	93	118	180	1	1
91001248	pm2708	9	TGTATTGGATTGGATTCTC	CAAAAGCAAAACAGCAGATA	44	95	95	-	85	1	1
91001655	pm0995	97	TTGCCATCAAAACACATACA	CTTGTAGTTTGGTTTCTG	43	55	55	-	-	1	1
91001157	pm0959	97	TTAAGAAATCACCCTCATTTG	CACATGCTTATGGAACT	44	74	74	72	73	1	1
91001268	pm0547	10	AAGTATGTGCAAGAGATGTA	AAGAAACACTGCCCTGTGG	45	138	139	>200	>200	2	3
91002278	pm2245	10	TGTGAATGCTATCTCTCT	GCATCTGTTCCATATCAGT	47	100	100	200	>200	1	1
91001159	pm2664	11	ATCAAAACAAACAAATCCAGA	AGTAAATATATCTGCAACT	42	117	121	134	95	2	2
91001315	pm0880	11	GAATAGCTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1
91001352	pm0445	11	AAAGTACCTTGTGACAGTGGGA	TCGAGCCAAATACATGCTGACT	50	153	153	>200	160	1	2
91001469	pm2943	11	AGGGTGAAGGGTATTTTACG	CACATCAGTTGAGAGCTA	47	83	85	-	-	2	2
91001570	pm2810	11	AACCTCTAGTAGGCATTG	TTATTAACCAATCCAGTA	37	47	47	125	53	1	1
91000279	pm0266	11	CTGTAAGAGTTTGGAAATATGT	TTTCAATTTCTACCAATTAAT	42	75,82	75	145	>200	3	3
91001163	pm2756	12	AGTGTATGGAAGACCTTGAG	GTTCATTTGAACGGGTAGC	48	130	130	103	>200	1	2
91001193	pm1193	12	TCTCCCTATTCACAGCAGT	AATGATTCGTAGGATAGCA	49	88	83	>200	120	1	2
91001235	pm2790	12	CACAGATAAAGAAATCATATA	ACCCTAATTTAGTTTCTCAG	46	100	100	-	-	1	1
91001274	pm1355	12	CATCATGGTACAGTCAGAG	CAGTTGTCAAAATGTAATG	44	83	82	91	87	1	1
91001274	pm1355	12	AGATGCTAGTATTCCTCATGG	GAGAACAGCAGTAAGCAACCAC	47	87	87	>200	>200	1	1
91001308	pm0368	12	CCAAAGTCTAGGGTACAG	TTCAATAGACCTTGGTTAC	47	95,165	95	>200	>200	1	1
91000158	pm2845	13	CTAAGATTAAATGCGATTC	AGTTAGTGTATGCCAGAGGA	46	104	104	>200	>200	1	2

F18. 8

g1.001014	pm1658	13	TGTAAAGCTATCAGAGTCA	AGCAGAGCTATGCCATCTA	44	109,200	109	>200	100	1
g1.001290	pm1721	13	GCTTCTCCGTGCTGTGGT	GCAGTTATCAGGCTATCTCC	50	122	122	>200	130	1
g1.001362	pm1710	13	ACTGAATGGAACTAGTCT	TACATCAGACATGTGA	40	61	61	85	101	1
g1.001366	pm1364	13	TGCTAGCTTCCCTCTTA	GAGCATTCCTGTTCTTA	45	67	67	-	-	1
g1.001369	pm2301	13	CATGAACCTGCTCAGACAA	GCCITACITTAATGCTGACC	51	100	100	>200	>200	1
g1.001402	pm1541	13	AAATGAATGTAATAGCACT	ATTAGTTACAGGGAGAAT	41	72	72	-	-	1
g1.001367	pm1411	14	GTTTAAAGTTTGAATTGGG	CATTCCACTCTACATTCTT	41	77	77	>200	100	3
g1.001564	pm2307	14	GGTTCCTAACTCGAAATC	AATGCTCAATTAATCTCAAG	42	55	55	>200	>200	1
g1.001576	pm2010	14	ATCACAATTACCTTGTAGTG	TCAGAACAAAGGAACCACT	39	69	69	-	-	1
g1.001330	pm2720	15	TCCCATCCTCAGTTGAAT	TCAGAACAAAGGAACCACT	47	70	70	00	150	1
g1.000960	pm1995	16	TGGAAATGGAAACCTTGCTA	ACTATGCTGCCGAAATGG	48	79	79	66	70	2
g1.001242	pm1127	16	CCCTTGTTTACATGTCA	TATTAATCTGCCAATCAT	44	105	105	103	102	2
g1.001516	pm2543	16	ACAGTCTTAAATCAAAGGTG	TCTGACACTCAAGTGGCAAT	45	70	70	>200	-	1
g1.001566	pm10913	17	TTTGTCGGACTATGTAAT	TCACITTTAATGGGAACCAAG	41	53	53	>200	>200	1
g1.000206	pm1157	17	CTCTCCATGTTCTACAAAG	TAGAAGGAGAAATCTGTGTT	47	77	77	140	>200	2
g1.001015	pm2360	17	ATATTCACCTTCCCATCCAT	TCATACTGCTCTCAAGC	50	80	80	>200	>200	1
g1.001156	pm1202	17	CAGAAATTAAGTGCAGCAAT	TCGTACTGCATCTTAAAT	45	103	100	>200	>200	2
g1.001173	pm2117	17	AAATCTGTGGTATTTCC	GTGATCTAGTGCATATGC	41	110	118	145	200	1
g1.001301	pm1070	17	TAAATTTGGAAATCTCTGGA	ACACATTTGGGTTTGCCTTAAC	45	120	129	-	-	1
g1.001316	pm10511	17	TGTGACAGCAGCAGCTCAT	TCGTACATTTAATCTCCACC	40	90	90	69	>200	1
g1.001356	pm2212	17	CATCTCAGACAAAGGAAC	ACCTAAGATCCAGAGAAAC	46	90	90	180	>200	1
g1.001405	pm10642	17	TACIGGCATAGGAGTTGT	GAACATACCACGTTATTCT	45	68	68	160	-	1
g1.001522	pm1015	18	GTCTCAGCAGTTTCAAGTT	ACTTCTCTTGAGGACACA	49	65	65	>200	>200	1
g1.001070	pm2309	19	TGTTCTCCAGCTTGTAG	GTTACATGCTTGGTACAG	46	50	50	-	-	1
g1.001467	pm1690	19	GGATCAGACCAACAGTGTCTG	GCAAGGTATAAACAGATTGA	54	93	93	>200	>200	2
g1.001069	pm1079	20	GAAGCCCAACCTGCACTCA	GGAGAGTATGGGGAACGGT	48	140	140	-	-	1
g1.001000	pm1146	20	GCCCTAGGATTCACTGCTC	TTAAGAAGCCATTAGCTAGGATA	52	66	66	180	>200	1
g1.001089	pm1012	20	TGCTGGATGACTCTACAGC	ACCACCAAGCTCTTTCAGG	49	59	59	59,115	58	1
g1.001120	pm1932	20	CTGCTGGCTAGTCTGACTC	TCCCTATCATGGCTGCTGTT	49	135	135	153	160	1
g1.001132	pm10647	20	TCTGAATGATGATGGAACA	CAMAAGGTCTAAGAGACAT	48	109	109	-	-	1
g1.001150	pm1774	20	GGAGCCACATGGATTGATTG	ATCCTAGTCCCAACCCAGTA	52	124	124	>200	>200	1
g1.001210	pm1235	20	AGCCATCTGGTTATGCTTA	AAATGTACCCCTGGCACCTC	44	90	90	>200	>200	1
g1.001295	pm2101	21	TCCATGGTGTAGAAGCCAG	GGAGCAGAAATGAACCTTAC	54	142	142	>200	74	1
g1.001427	pm10640	21	CTCTGCTATAAAGTAGAG	CCACATCTCCACAGGGAGT	45	130	130	180	>200	1
g1.000370	pm1912	22	GGTGTAGTGTAAACATTAG	ACAATGGTCTACTAAATGA	39	50	50	145	>200	1
g1.001444	pm1911	22	GGTCTGTCTCCCATCTGT	AGTTGCACCCATCTCTGTC	46	124	124	>200	>200	1
g1.001473	pm2231	22	TGAGCTGCATCTACCTGTGAGG	AGAAAGCCCAAGAGTAGTCC	48	65,80	65	100	125	1
g1.001479	pm2320	22	TACAGCCCTCCCAAGCTAAAC	AAGCAGGTGAGTGGGTCTTCT	50	94	94	67	135	2
				TTTATCTGCAATCCACTACAA	46	65	65	190	>200	1

Fig. 9

91000999	pin1759	X	CTCCATAGTACCTGGATT	TCACCCACCACTATTAGCA	47	103	103	-	-	-	1
91001119	pin2160	X	GGAGGGAGATATAGATTGT	AAAAATCCAGAGACTGA	46	70	70	135	130	-	1
91001161	pin0508	X	TTCTATAGTGTGACCGTT	GGAGGATTGAGATACAT	40	85	85	>200	77	-	1
91001104	pin1291	X	TATGCCAGTGAATGTTCGTAA	GTAAAGGTATCTTGCATCAGA	47	02	02	>200	80	2	3
91001168	pin2289	1,10	ATCTCTGTAATATACATCG	GGGGAGAGACATCACATGAC	46	70	70	68	130	-	1
91001136	pin0113	1,2,12,13,Y	GATCCGATGAGAGTGAAT	AATACAAAGCTAAACCACAA	44	69	69	170	-	-	1
91001104	pin2272	1,2,3,5,8,12,14,17,X	TTGGATTCACATCTCTAT	TTATGTGTACAAAGCACT	43	130	130	150	132	2	2
91000303	pin0314	1,2,6,X	TATCAGCTGAATATGTCAC	TTACTGAATCCAGCCAACCA	45	93	93	110	-	-	3
91000140	pin1481	1,3,4,5,8,10	TCCAAATGAAGAGGTGTA	AGTTCACAGCCAGGTGAATG	43	06	06	100	100	1	3
91001354	pin1361	2,20,21,22	GTCTGTAAGCCAGATTC	TTTTTATGTGCTCCAAGT	43	110	110	170	150	-	1
91000376	pin2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATAGTGTGTACACTCG	43	61	61	-	-	-	2
91001077	pin0913	2,5,14,C	GCCTGTGTATTCACCCTG	ATCTCCCTTGTCTCCAGTTA	46	82	82	>200	82	-	6
91001192	pin1653	2,8,12	TCTGAGGACATTCGAAGCAG	CAGTCAAAACCAACACGGTAT	49	95	95	93	160	-	1
91000213	pin1778	2,9,13,17,X	TGCATAAGGGGAAGACCA	CCGTGTAGGTGATGAATG	49	78	80	>200	>200	-	1
91000918	pin0885	20,X	GTCAATTGTATGCAATTTC	ACATTATATTTTTCACCG	37	45	45	-	-	-	2
91001109	pin0457	3,10,15	CATGTACTCAGAGGCATTC	GCACTACAAATCCCAACT	50	133	133	>200	150	2	2
91000071	pin2651	3,4,M	CAGGACTGGAGCGAGGAAG	GATTTACCCATAGGAAGC	50	101	101	101	88	3	3
91001126	pin2632	3,6	TTAGGAAATATGTTAGACAG	ATAGTATGGGTGTACACAGTA	43	00	00	>200	170	-	1
91001191	pin1133	3,8	TGGATTGCTTTACTCTGTT	ACACCTCAGGAGATGTTAC	47	93	93	95	>200	-	1
91000377	pin2750	3,9,10,15	GCATCAACAGCCAAATCAGA	CTCTTACCAACCAACAGCAG	50	96	96	>200	175	2	10
91000603	pin0626	4,6	GGATTCTCTTGTGTCAT	GTTTATGTACGGCATTAC	44	105	100	>200	>200	2	4
91001212	pin1234	6,20	GCATTAAACAGGAAACAATA	CTGTCCAATGTGCTAAAC	44	110	110	105	107	-	1
91001312	pin0606	7,18	AGATGCTACATTAGGGATA	TTTTAGACATACAGAGAGT	43	81	81	102	-	-	1
91001111	pin1253	8,11	CCAGACTACAGGCTGATGGC	CCCTTACCCCAAGCACTCTT	55	75,130	75	>200	>200	-	1
91001357	pin0115	9,M	ACCAAATGTCACCTGCTTAAATA	CCCAATAAGTGAAGAGTACTTC	48	125,155	127	125	>200	-	1
91001264	pin0128	10,15,22	AAGAAATGTTTACTGGATT	TTATCTGACTTGGAGAAAT	42	107	107	-	-	-	1
91001154	pin2120	10,15,22	ACTACCCCTGAGATATAGTT	TTCAITTTATTTATAGTTGA	46	100	100	170	-	-	1
91000750	pin2303	11,M	ATACCACTCCGCTGTTCACG	GAGGAGCTCTACTGGTCTT	50	72	74	72	>200	3	20
91000314	pin2613	12,19	GCACCAAGAACGAGTCCAG	TTGGGAATGAGAAAATAACT	46	83	83	81	-	-	3
91000103	pin2773	12,M	GATCTCAGTCTGCGTTTAT	TACATACAAAGATGCCAACAGT	44	00	00	79	68	-	1
91001187	pin2725	13,16	ATCTGTGTGCTGCTTCC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	-	1
91000976	pin2780	14,16	AACCTGTTTACCCGATCTT	AGGTATTTGTCCACCAGAA	48	87	87	>200	>200	-	1
91001135	pin1683	17,20,C	TGTGGTTCACCATTCAGAC	AGAACACACATCAAAAGATGC	46	90	90	>200	00	-	1
91001193	pin1740	17,22,Y	GAAATGATCCCAAGAGCTAG	CTAGTTATCTCTGGCTCTG	44	81	81	>200	200	-	1
91000566	pin0564	17,C	TTTATCCCAAGCAAGCAAC	TCCTCTCTCTCTCTCTCTC	40	120	120	>200	170	4	11
91001369	pin2217	17,C	ACTTAAAGTAGCTTTGTACG	TGCCCTCTCTCTCTCTCTCT	43	95	95	>200	95	-	1
91001160	pin1213	18,C	CCCCAGTTAAGGATATGTT	AGTGACGATGGAGGAGTGA	44	92	92	-	92	-	1
91001117	pin1118	19,20	TGCAGAGTGATTTCCAGAG	CGTAGGCTATCTTTCACG	46	75	72	160	65	-	1
91001009	pin2024	19,22	ATCCCTCTCTCTATTCACAC	GCCTGTTTAACTCACATCAC	46	110	110	130	170	2	2
91001172	pin0887	19,22	GCCTGCATCTGTGTGACTT	AACCTCTGGGAACAAATCAT	48	91	89	160	86	-	1

Fig. 10

g1001057	pml2040	C	AGACACAAACACACAGCTAT	TTTTCTGATTATGACATGAC	45	75	75	101	75	1	1
g1000173	pml1753	N	ATCTCTTTGAGCCATCTGT	GTAAAGTGTGATGCCATT	42	64,100	64	64	>200	1	1
g1001096	pml2230	N	GTAGAGCTGCATTGACTACC	ACAGACAAGGAATAATCATTA	42	100,96	110	110	112	1	1
g1001166	pml500	N	GTCCACAGTCCAGCTAAC	GCCACATATAGAAATCCATC	46	74	74	74	>200	1	1
g1001151	pml2351	N	TGCTTTGTGACTCTGCT	TTTAAACAGTCAATAATACATGTT	44	110	110	110	106	1	1
g1000370	pml2402	M1,C	GCTAGAAAGAGGGCACTCA	CTTAACCTGATAGCCAGTTC	46	75	75	75	75	1	1
g1000353	pml2706	M1,C	CACAAAACAGCAACTTCAG	ATGGTTATTTATCAATTC	41	83	83	82	81	2	3
g1000265	pml1704	M1,C	TCCACCACAGAGAGCACACT	AATTCATAGGGAATAGGTTTC	40	75,130	75	75	75	1	23
g1000313	pml2310	M1,C	TGCAGAGGACCAAAATCAC	GAACAGGTTAGTCCATTCG	40	50	50	58	50	1	1
g1000575	pml1609	M1,C	CATGAGGCTACGAAACAGG	AGGAGTCCGTGGGTCTGAG	51	81	81	84	84	4	18
g1000732	pml1442	M1,C	AAAGCATCTGAGAGGAACA	GGAGGACTCGCTTGGTCTTA	49	110, >200	110	110	110	1	8
g1000995	pml152	M1,C	GCAGCAATACCTTACACC	TGGTTTCATTTCAGTTCCTTC	51	102	105	102	102	3	13
g1001016	pml2760	M1,C	GAAGCTCTGTGAGGAAAGT	CAGACCCATCTTTATACC	47	79	79	79	79	3	4
g1001127	pml1144	M1,C	ACGATATTTATAGTAGTG	TCAAACTTTAATATATGCT	40	93	93	91	92	1	1
g1001167	pml2290	M1,C	AGATGAGTGTGGTTCAGAGA	CCATTCCTGTCTATCCAGTT	52	135	140	135	135	1	1
g1001216	pml1626	M1,C	GAGAGCCCTTGCATCCCTTA	CTCCCTTTGGTCTTCTGT	47	55	55	55	55	1	1
g1001353	pml2100	M1,C	TAAGTCAGAGATCAGTAAGT	ACATGATTTTATATATGCT	49	100	100	100	100	1	1
g1001375	pml1240	M1,C	AACTGGTCCATCAAGACTG	AGTGAATAAACTCTCCATCC	42	110	110	110	110	1	2
g1001375	pml131	M1,C	ACTTAAAAACCCACACAGAT	ACAAACAGCAGTCAAAATAGAA	48	120	120	120	120	1	1
g1001356	pml0952	M1,C	AAGAGGAGTTTCCCTGCTCA	ATCATGACAGATGGCAAGGA	47	97	97	97	97	1	1
g1001111	pml2216	M1,C	ATCTGCATGAGCTATATCT	CGTCTCTTTTATTTGACAT	51	89	89	89	150	1	1
g1001460	pml0950	M1,C	ATGGGTTATCAGAGGCTTTC	CAGACCAAAAGCACCTCTTA	45	100	100	100	100	1	1
g1001402	pml2026	M1,C	ACATGGAATGGGATGAGGT	GGACATTTCTAGCCACAGC	47	80	77	80	80	1	1
g1001150	pml1210	M1,C	TTGTTGACATTCCTTTTAGAA	CAGTCCCTCTGTACTGAGACA	51	75,55	75	75	75	1	2
g1000160	pml0100	M1,C	GCCCACAGACATCATCCT	TCTTAGTAGGTGCTCTGGTG	46	85	85	85	85	1	2
g1000050	pml2042	No product	CAACCAATAGGCTGAAAGT	GAAATAATCTGTCTCATCTA	45	87	87	87	87	1	1
g1000260	pml304	No product	CTTTGGGATATTTCTTCAT	CCCTCGGGTACTTTCTATG	43	60	60	62	62	1	2
g1001354	pml0800	No product	AGCCAGCCCTTTGTATGTG	CTGGATTGATTTTCATAG	44	87	87	87	112	1	1
g1001365	pml1073	No product	TGTTGGTATGAAATATCTGA	TTATGAATGAGACAAACACT	43	98	98	103	>200	1	1
g1001373	pml2900	No product	CAGTAGTGTGCTTTGAAATG	TTATGTAATATGTGCTGT	41	63	63	63	150	3	3
g1001556	pml0361	No product	TACAGCCGCTCTAAAGTGC	TTTGAAGATCAAGGAAATCT	48	82	82	82	>200	1	1
g1001574	pml0449	No product	TACATTCCTCAGAGCTCATGC	TTTCAAAACTTTATCTCT	40	86	86	86	>200	1	1
g1001622	pml1284	No product	ATCAGAGCTCAGTCTCTAG	ATTTCCTCTGCTATGGTG	44	57	57	57	67	2	2
g1001640	pml1606	No product	GATCTTGAGCCCTAACGGA	TTTGCAGTTCAGCTTATTC	45	54	54	54	54	1	1
g1001640	pml0952	No product	GATCTCTGTTCTTTTCACA	TTTATACAGACACCACTAC	36	45	45	45	45	1	1

Fig. 11

pm2209 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y H H C N

Fig. 12

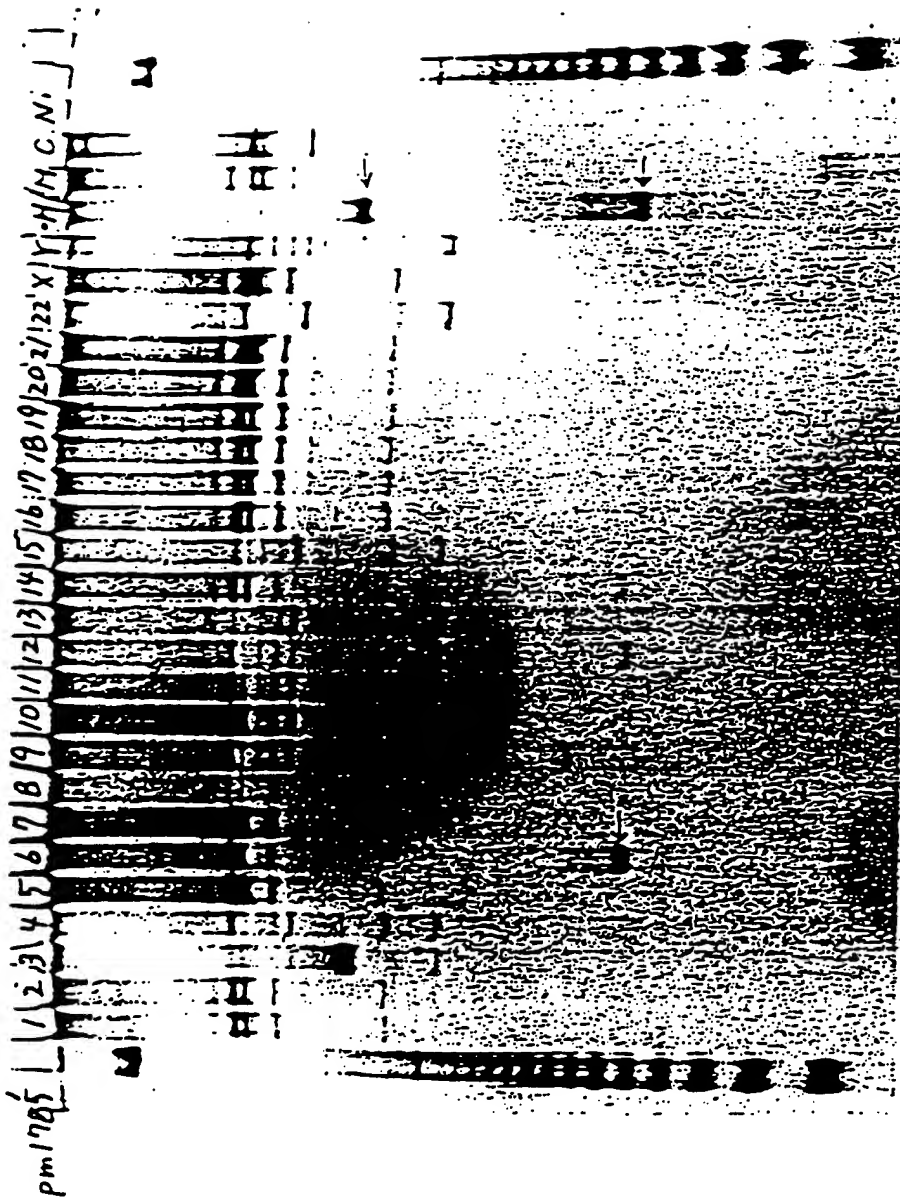


Fig. 13

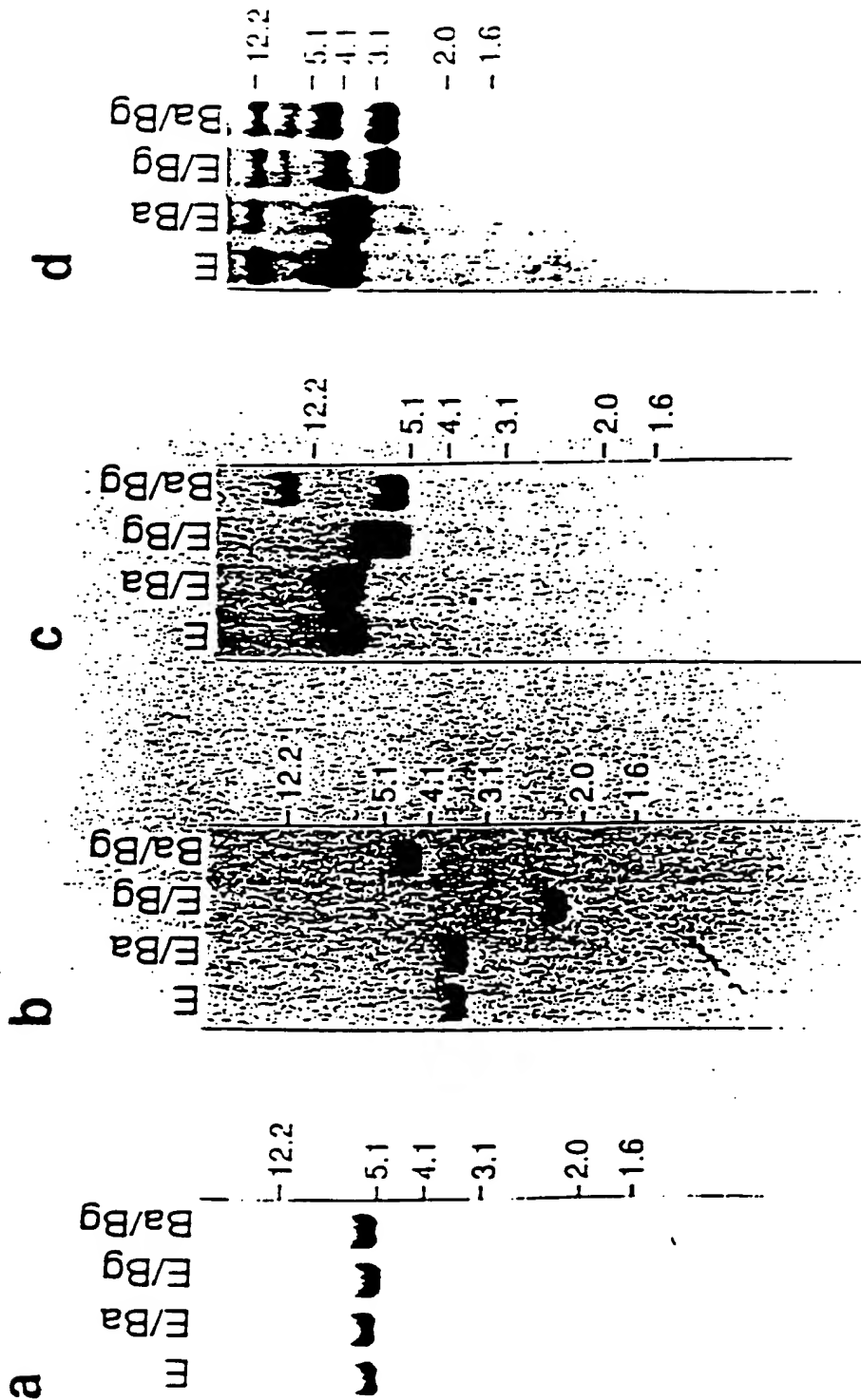


Fig. 14

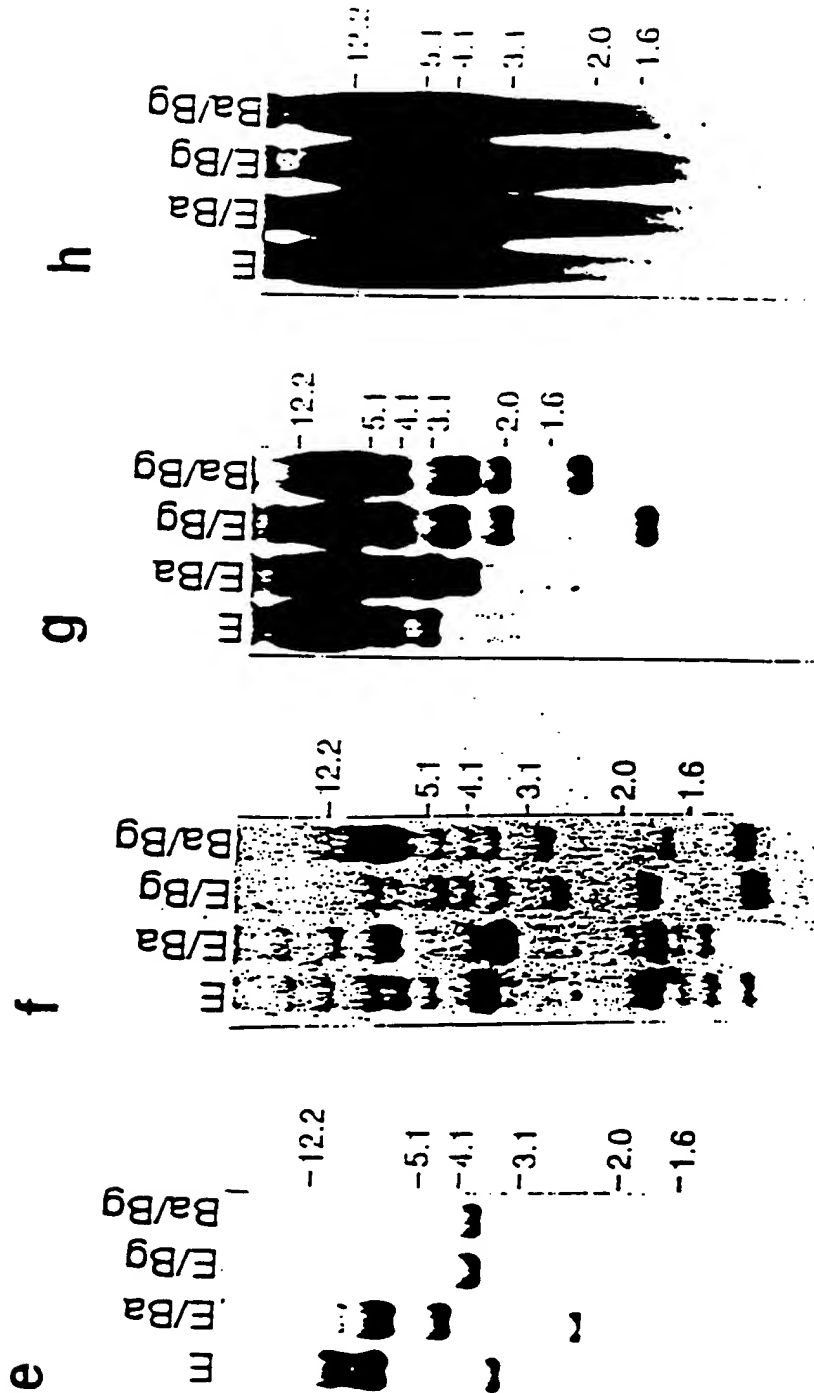




Fig. 15

## Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (3)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	73
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

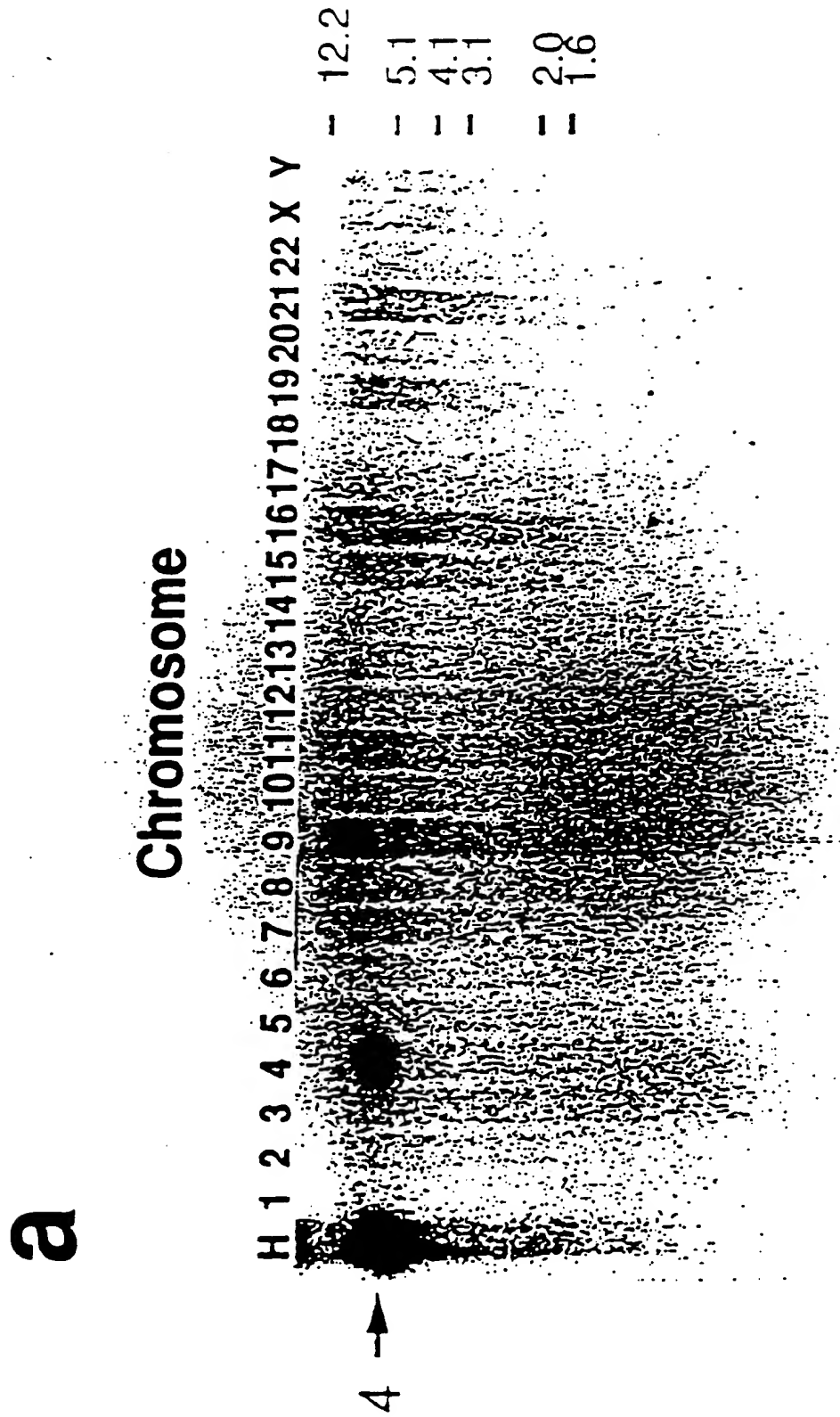


Fig. 17

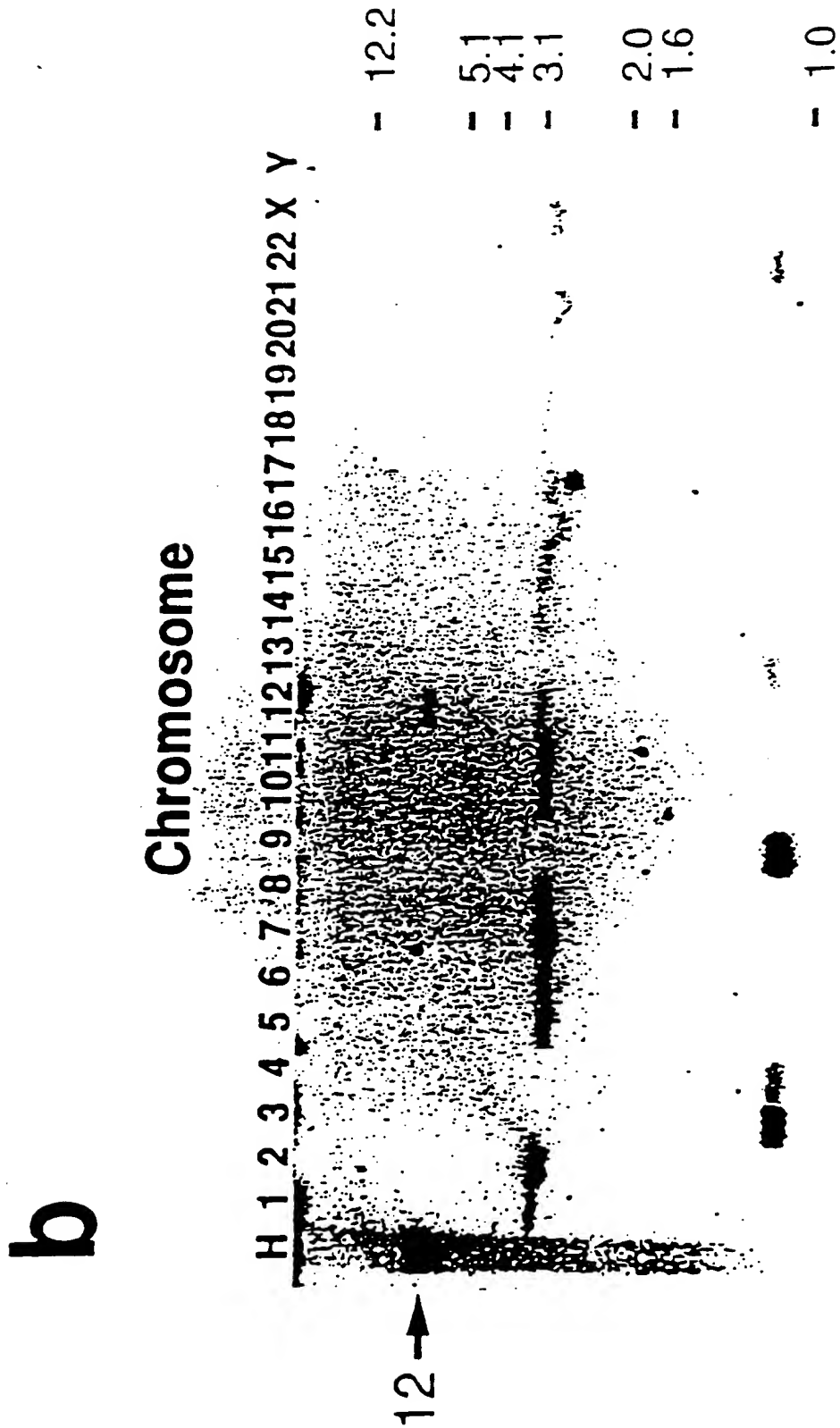


Fig. 18

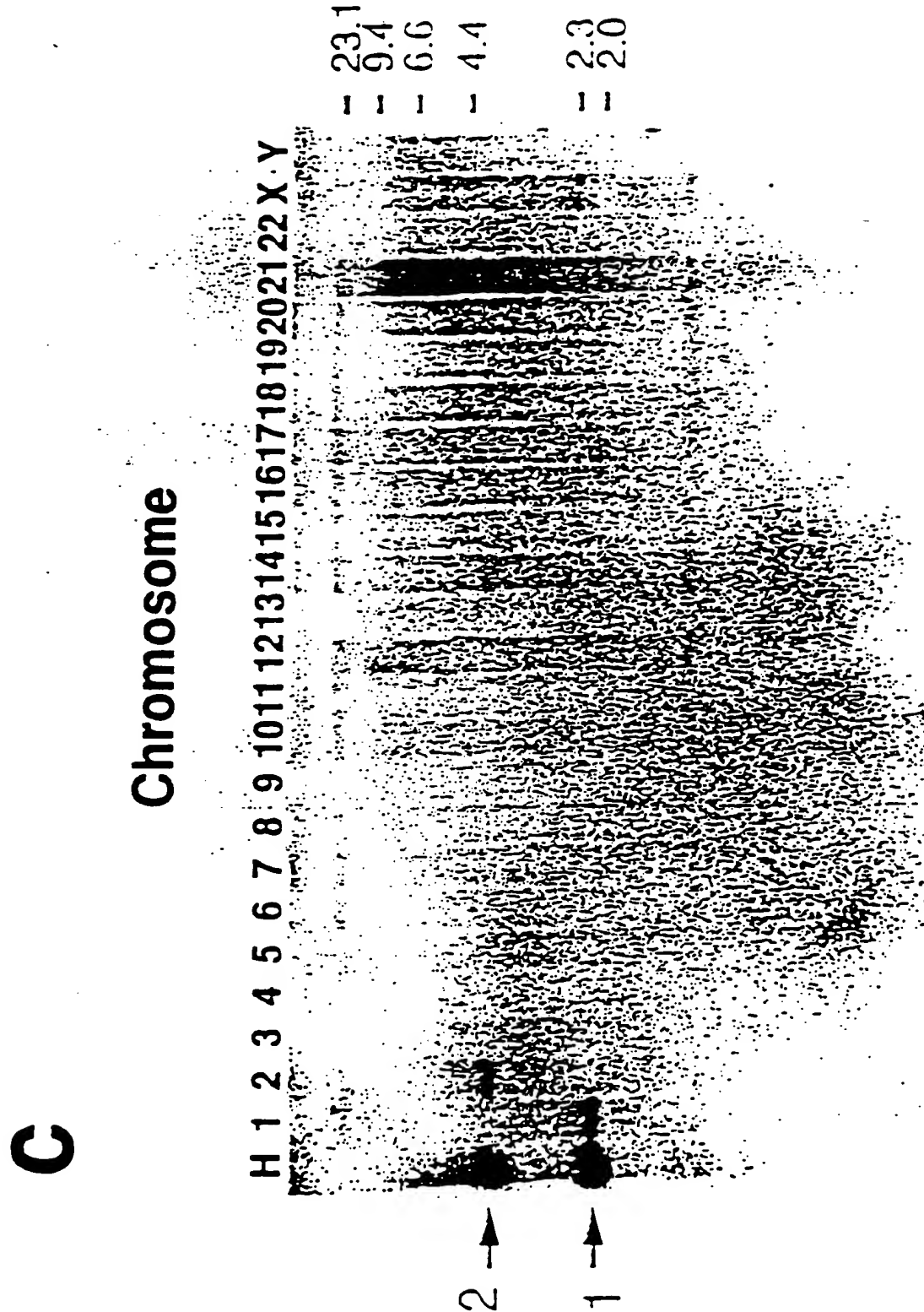


Fig. 19

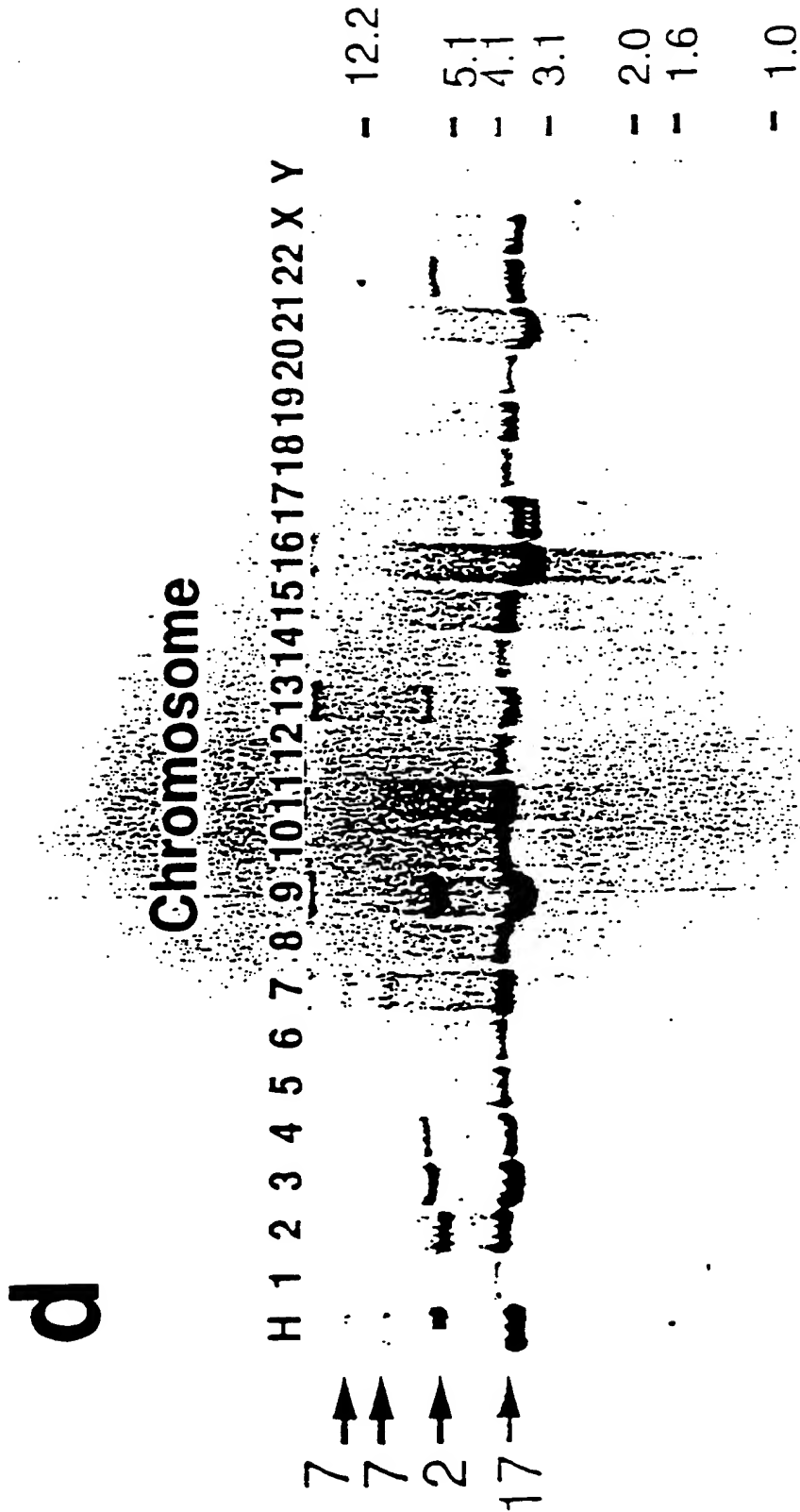


Fig. 20

e

# Chromosome

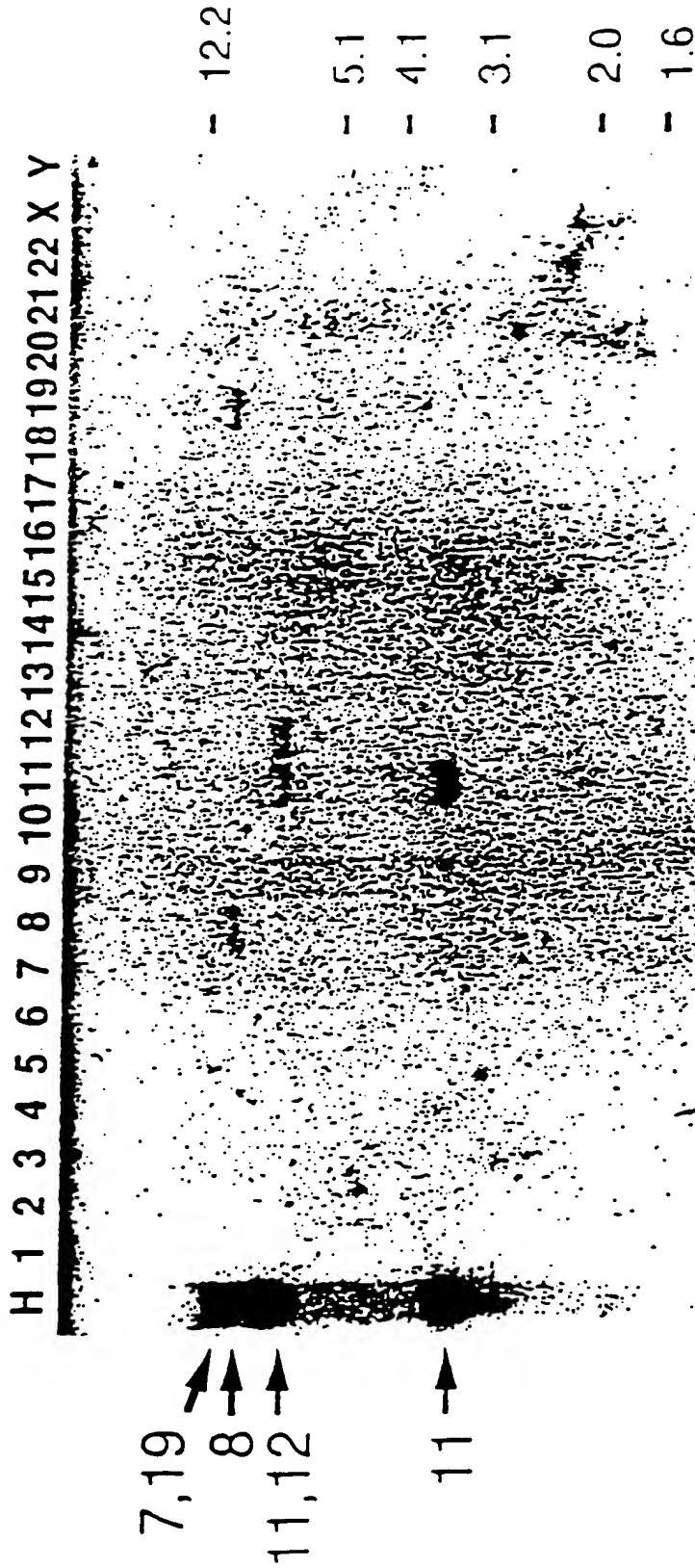


Fig. 21

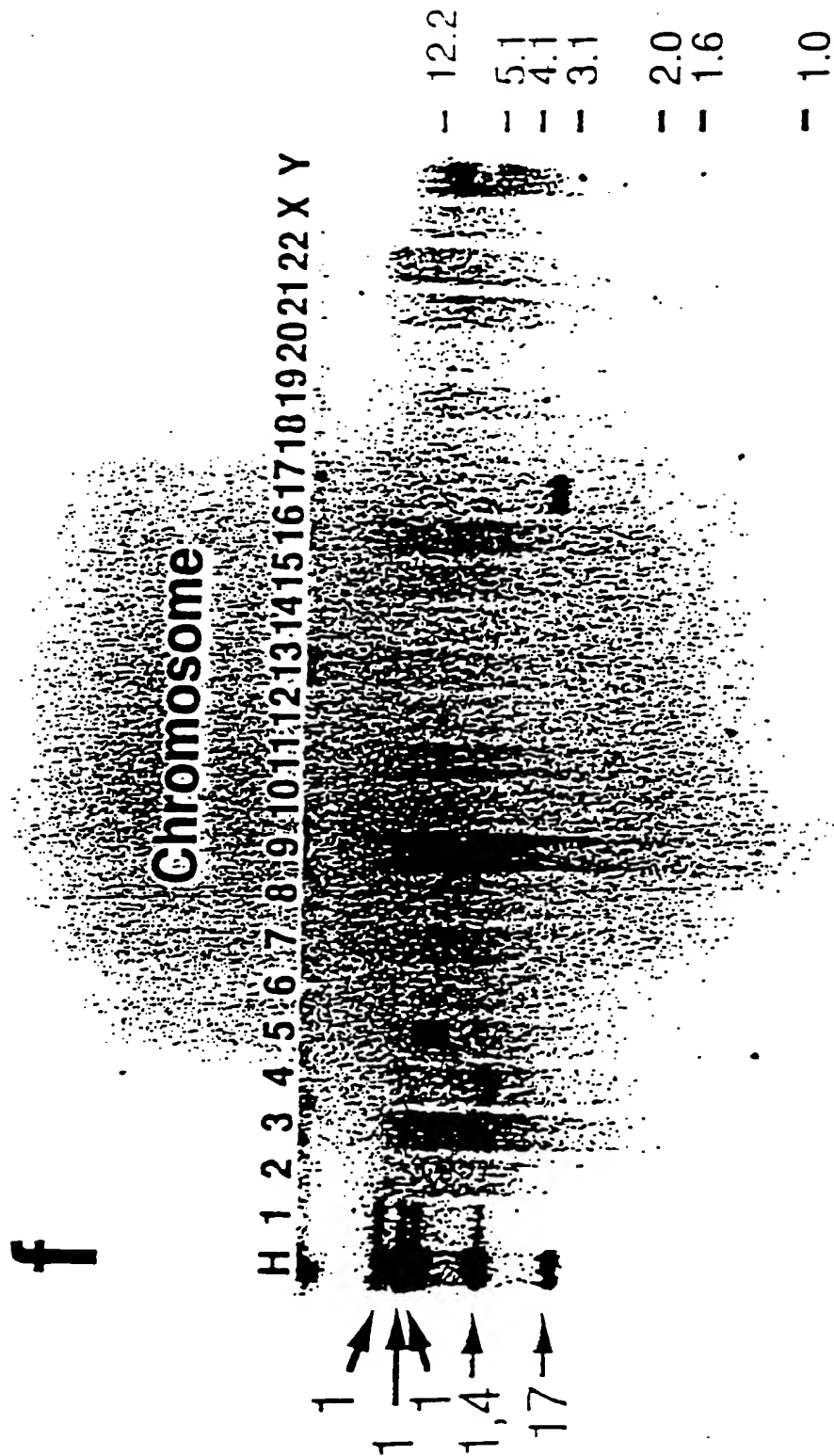


Fig. 22

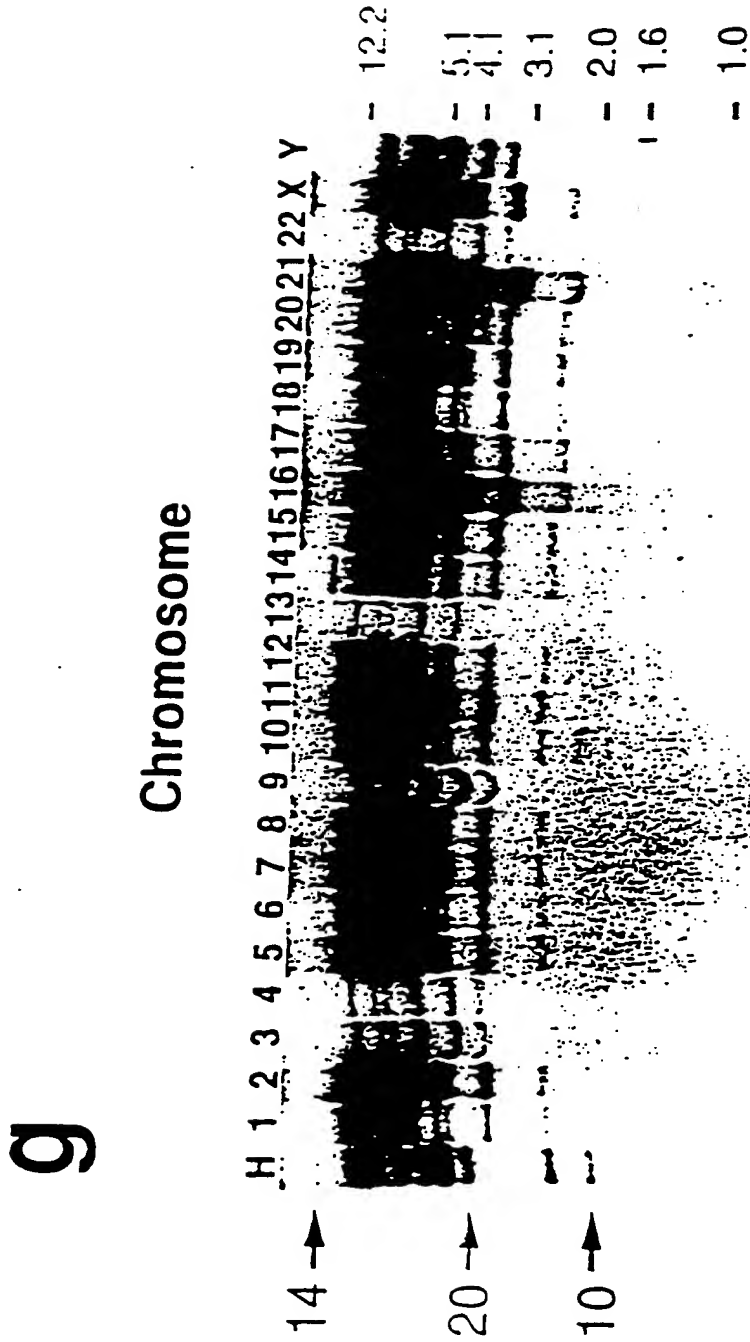




Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes		Chromosomes assigned						Background	
Clone	Sequence length ±	2/3	3/3	3/3	3/3	3/3	3/3	Mouse	Chinese hamster
Single band group:									
c12c11	GS000075	432	1	1	1	1	9	0	0
c12c06	GS000062	540	1	1	1	1	5.15	0	0
c12g01	GS000290	212	1	1	1	1	2	1	1
c13c05	GS000117	359	1	1	1	1	11-	0	0
c13c07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	257	1	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	1	12-	0	0
c13h02	GS000322	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000134	313	1	1	1	1	11	1	1
d1b10	GS000344	151	1	1	1	1	20	0	0
hm01c12	GS000223	246	1	1	1	1	27	0	0
hm01c09	GS000423	157	0	1	1	1	1	0	0
hm01c12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02c01	GS000293	271	1	1	1	1	15	0	0
hm02c01	GS000015	590	1	1	1	1	20	0	0
hm02c02	GS000342	156	0	1	1	1	14	0	0
hm02c05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	1	17	0	0
hm05c05	GS000251	219	1	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1	1
hm05c10	GS000009	606	1	1	1	1	1	0	0
kmc01	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000057	471	1	1	1	1	3	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000259	204	1	1	1	1	3	0	0
s147	GS000050	461	1	1	1	0	2	0	0
s14c06	junk	619	1	1	1	1	1	0	0
s14g02	GS000132	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000224	241	1	1	1	1	9	0	0
s247	GS000347	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Numbers of bands detected with human whole chromosomes			Chromosomes assigned				Background		
Clone	Sequence length	$\Sigma$	$\Sigma/91$	$\Sigma/35$	$31/35$		Mouse	Chinese hamster	
s306	CS000256	203	1	1	0	1	X	0	0
s309	CS000171	303	1	1	0	1	1	0	0
s342	CS000323	163	1	1	1	1	4	3	2
s331	CS000255	207	1	1	0	1	6.13	1	1
s334	CS000165	312	1	1	1	1	1	0	0
s337	CS000276	193	1	1	1	1	17	0	0
s339	CS000295	130	1	1	1	1	a.d.	0	1
s443	CS000330	231	1	1	1	1	a.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	CS000192	273	1	1	1	1	3	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	CS000334	141	1	1	1	1	14	1	1
s632	junk	387	1	1	1	1	2	0	0
s633	CS000166	311	1	1	1	1	22	2	1
s650	CS000041	644	1	1	1	1	12	1	1
tw1-04	CS000025	337	1	1	1	1	3.7	0	0
tw1-19	CS000218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	CS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-43	CS000098	178	1	1	1	1	14	0	0
tw1-96	CS000138	339	1	1	1	1	11	0	0
Two band group:									
e12212	CS000195	277	1	2	2	2	1.	1	1
e13402	CS000042	303	2	2	1	1	2.	0	0
hm01a06	CS000129	344	2	2	2	2	11.13	3	3
hm01a07	CS000207	249	2	2	2	2	7.	0	0
hm01d05	CS000232	243	2	2	2	1	2.	0	0
hm01e01	CS000181	292	2	2	2	2	1.2	0	0
hm02a08	CS000435	302	2	2	2	2	3.	1	1
hm02e04	CS000221	253	2	2	2	2	3.	0	0
hm02e05	CS000146	332	2	2	2	2	17.19.22	0	0
hm03f07	CS000043	303	1	1	2	1	3.	0	0
s11d06	CS000268	203	2	2	2	2	11.12	0	0
s11g12	CS000337	233	2	2	2	2	6.	0	0
s124	CS000083	404	2	2	2	2	9.	1	1
s144	CS000132	342	1	2	2	2	1.7	0	0
s14f03	CS000239	243	1	2	2	2	2.	3	2
s15e02	junk	439	2	2	1	2	6.	0	0
s16b09	junk	420	1	1	1	2	10.14	0	0
s17e09	CS000248	223	2	2	2	2	14.	0	0
s231	junk	284	2	2	2	2	11.	0	0
s234	CS000124	353	2	2	2	2	1.	3	1
s253	CS000235	239	2	2	2	2	11.	0	0
s272	junk	193	2	2	2	2	10.16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes			Chromosomes assigned				Background	
Clone	Sequence length	5	5/8	5/9	5/10		Mouse	Chinese hamster
s311	CS000092	333	1	1	2	2	16.	1
s313	junk	132	2	2	1	0	20.	0
s317	CS000100	339	0	0	1	2	14,14	1
s336	CS000134	337	2	2	2	2	12,14	0
s333	CS000139	233	2	2	2	1	22,X	0
s339	CS000233	137	2	1	1	2	17.	0
s394	CS000063	449	2	1	2	2	13,14	0
s396	junk	277	2	2	2	2	17.	0
s455	junk	452	1	2	2	1	4.	0
s456	CS000236	132	2	2	2	2	8,10	1
s465	CS000201	374	1	1	2	2	6,15	0
s615	junk	250	1	1	1	2	9,13	0
s639	CS000257	205	1	2	2	2	2X	0
s656	CS000025	590	2	2	0	2	6,11	0
twl-33	junk	352	2	2	2	2	1.	0
twl-39	CS000153	321	2	2	2	2	17.	0
twl-70	CS000061	441	1	1	2	1	11.	0
twl-80	junk	453	2	2	1	2	9,17	2
twl-87	CS000152	316	2	2	2	2	7.	0
Three band group								
d0h06	CS000030	417	3	3	3	1	1.	0
hm05b07	junk	336	2	3	3	3	5.	0
hm05g02	CS000209	267	2	2	2	1	5,17,19	1
s129	CS000107	373	3	3	3	3	n.d.	1
s173	CS000257	146	1	2	2	3	2.	0
s17s10	CS000294	131	3	3	3	3	2,13,22	1
s308	CS000412	633	2	2	2	3	XX	1
s401	CS000224	249	2	3	3	3	6,5.	0
s654	CS000045	491	3	3	3	3	1,22.	0
twl-82	CS000202	267	3	3	3	3	13.	4
Four band group								
cl2g07	CS000154	320	4	4	2	3	5, 14.	0
cl3a08	CS000055	508	3	3	4	4	2,7,7,17	1
cl3c04	CS000106	376	4	3	3	3	n.d.	0
cl3c09	CS000302	195	4	2	4	4	2,17.	7
s136	CS000160	315	4	4	4	4	4X	2
s163	CS000004	618	4	4	4	2	4,4,8,20	3
s479	CS000130	293	4	4	2	2	7,5,11,11,12,19	0
Group with 5 or more bands								
cl2f08	CS000253	217	5	5	5	2	2,7,9,14.	2
hc01	junk	374	12	12	13	13	1,2,6.	22
hd10	junk	361	4	4	4	8	n.d.	12
he10	junk	173	6	2	3	3	6,3,9,19,21.	3
hm01c05	CS000205	176	9	7	5	5	X	9
hm01f04	CS000246	215	8	10	5	5	n.d.	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14

Fig. 26

Numbers of bands detected with human whole chromosomes				Chromosomes assigned			Background		
Clone	Sequence length	≡	≡/≡ <sub>1</sub>	≡/≡ <sub>2</sub>	≡/≡ <sub>3</sub>		Mouse	Chinese hamster	
hm02f09	CS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm03a02	CS000096	373	5	6	4	6	2,3,17.	3	3
hm03a04	CS000236	3239	6	6	6	7	a.d.	2	5
km501	junk	350	3	5	5	5	13.	14	7
s11f06	CS000316	170	6	6	6	4	1,2,2,3,4,6,13,15.	0	3
s14f01	CS000407	252	12	11	10	9	1,5,9,13.	6	3
s175	CS000094	397	5	4	4	3	1,1,1,1,4,17	0	0
s265	CS000223	167	10	12	11	14	13.	9	5
s341	junk	494	9	9	8	6	a.d.	15	3
s406	CS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X.	3	5
tw1-63	junk	203	8	10	10	12	3,4.	17	11
Bands no detected:									
cl3g02	CS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	CS000274	196	0	0	0	0	-	-	-
s323	CS000273	194	0	0	0	0	-	-	-
s339	CS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	CS000012	2734	0	0	0	0	-	-	-
s647	CS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

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## A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
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☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

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Date of the actual completion of the international search

February 6, 1995 (06. 02. 95)

Date of mailing of the international search report

March 7, 1995 (07. 03. 95)

Name and mailing address of the ISA/

Japanese Patent Office

Facsimile No.

Authorized officer

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Category <sup>o</sup>	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
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X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
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International application No.

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Category <sup>o</sup>	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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International application No.

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Hla, T. et al. "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors" p. 9308-9313	1-6 (2600)
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X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

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International application No.

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Category <sup>a</sup>	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
X	Nucleic Acids Res., Vol. 20, 1992, Wintzerith, M. et al. "Sequence of the human RNA polymerase II largest subunit" p. 910-910	1-6 (3083)
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X	Nature, Vol. 352, 1991, Maslen, C. L. et al. "Partial sequence of a candidate gene for the marfan syndrome" p. 334-337	1-6 (3334)
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X	J. Biol. Chem., Vol. 263, 1988, Wermuth, B. et al. "Human carbonyl reductase: Nucleotide sequence analysis of a cDNA and amino acid sequence of the encoded protein" p. 16185-16188	1-6 (4033)
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X	Nucleic Acids Res., Vol. 13, 1985, Hallewell, R. A. et al. "Human Cu/Zn superoxide dismutase cDNA: isolation of clones synthesising high levels of active or inactive enzyme from an expression library" p. 2017-2034	1-6 (4110)
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X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

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